

GenCore version 4.5						
Copyright (c) 1993 - 2000 Compugen Ltd.						
OM protein - protein search, using sw model						
Run on :	May 8, 2002, 11:08:20	Search time	13.29 Seconds			
Sequence :	1 MARDHHHHQDKKTMNNEE.....	alignments	1467.697	Million cell	updates/sec	MLGWHTRPLIATSAWKLSTN 532
Title:	US-09-911-513-2					
Perfect score:	2758					
Scoring table:	BLOSUM62					
Scorers:	Gapop 10.0 , Gapext 0.5					
Searched:	100059 seqs, 36664827 residues					
Total number of hits satisfying chosen parameters:	100059					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	SwissProt_39.*					
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
8						
Result No.	Score	Query Match	Length	DB	ID	Description
1	112.5	4.1	772	1	NFL1_HUMAN	Q14494 h. nuclear f
2	107	3.9	1158	1	CND1_SHRPO	Q94679 schizosaccharomyces pombe
3	106.5	3.9	1420	1	YAB2_YEAST	Q03496 sacharomyces cerevisiae
4	106	3.8	3206	1	POLG_PSEMV	P29152 p. genome pombe
5	104.5	3.8	953	1	IKA3_PSHAA	P55116 pastorella
6	104.5	3.8	4568	1	DTHC_CABEL	Q1020 caenorhabditis elegans
7	102.5	3.7	953	1	LKAB_PASHA	P55118 pastorella
8	101.5	3.7	580	1	RUBA_CHURE	Q42694 chlamydomonas
9	101.5	3.7	953	1	LRAL_PASHA	P16535 pastorella
10	101	3.7	414	1	SPYA_CALJA	P01029 calithrix
11	100	3.6	1007	1	MA2B_FELICA	Q46432 calithrix
12	99.5	3.6	1181	1	Y102_MEIJUA	Q60301 methanococcus
13	99.5	3.6	1436	1	DPO3_SPRAU	Q52665 staphylococcus
14	99	3.6	414	1	SPYA_FELICA	P14189 feline silvaticus
15	99	3.6	636	1	PHBC_RHIBET	Q27278 r. poly-beta
16	98.5	3.6	558	1	ORC2_XENLIA	Q19628 xenopus laevis
17	98.5	3.6	4590	1	FATH_HUMAN	Q1451 homo sapiens
18	97.5	3.5	1013	1	A6D_DROME	P21927 drosophila
19	96.5	3.5	761	1	POOF_KLEPN	P27508 klebsiella
20	96.5	3.5	851	1	OBP_HSV1	P10193 herpes simplex
21	96	3.5	350	1	SUDA_PIG	Q19069 sus scrofa
22	96	3.5	546	1	PGMU_ECOLI	P36938 escherichia
23	96	3.5	787	1	Y091_CABEL	P18422 caenorhabditis elegans
24	95	3.4	527	1	TCPB_SHRPO	Q10047 schizosaccharomyces pombe
25	95	3.4	665	1	ATKB_THEAC	P57700 thermoplasm
26	95	3.4	1549	1	GLSF_CYACA	Q19906 cyanidium
27	94.5	3.4	614	1	Y156_ARCFU	O28422 archaeoglobus
28	94.5	3.4	1260	1	YAOB_SHRPO	Q10093 schizosaccharomyces pombe
29	94.5	3.4	1597	1	CPTO_MOUSE	P49025 mus musculus
30	94	3.4	1071	1	CARB_BACSU	P25994 bacillus subtilis
31	94	3.4	4563	1	APP_HUMAN	P04114 homo sapiens
32	93.5	3.4	877	1	DPO1_SPRVIN	P33252 streptococcus
33	93.5	3.4	1330	1	VCOP_PRVTS	Q00705 esendordarie

FT	DOMAIN	682	704	LEUCINE-ZIPPER.				
SQ	SEQUENCE	772 AA;	84703 MW;	C8688076046BEF5	CRC64;			
<b>Query Match</b> 4.18; Score 112.5; DB 1; Length 772;								
Best Local Similarity	20.8%	Pred. No.	1.7;	CC8688076046BEF5	CRC64;			
Matches	118; Conservative	64; Mismatches	181; Indels	205; Gaps	27;			
QY	55	MSNVQEDDLQLATEVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIGDAILNQEA	114	CC	-1- FUNCTION: REQUIRED FOR CHROMOSOME CONDENSATION IN MITOSIS.			
Db	83	LTSQVRLDRQVPT-----TEVNAW-----LYHRDPEGS-----VSGSQPNGLA	123	CC	-1- ESSENTIAL FOR VIABILITY.			
QY	115	LSQSSNQGGGGDTYTNNRKCGSNGVYVETATAESTRHWLVLDSQENGVRVHALIA	174	CC	-1- SUBUNIT: PART OF THE CONDENSIN COMPLEX.			
Db	124	LESSGLQDVTGPD-----NGVRESETBOGFGF-----DLEDIG-----A	158	CC	-1- SUBCELLULAR LOCATION: NUCLEAR, AND CYTOPLASMIC (DURING			
QY	175	CAEVQ----KENLTVAEALVKQIGFLAVSQIGAMRKVATYF-----	212	CC	-1- INTERPHASE).			
Db	159	VAPPVGSDLITKEDIDLILWRQ-----DIDLGAGREVDYSHRQEYKELRDGGEQ	213	CC	-1- SIMILARITY: BELONGS TO THE CONDENSIN FAMILY.			
QY	213	-----ARALARRY-----RLSPSQSPIDH-----SLSDTLQMHFVETCPYLKFAHF	254	CC	-----			
Db	214	DTWAGEGALARNLNLYDGETGESPAQVPSQGEDQTALESLECPFGNAEFL	272	CC	-----			
QY	255	TAN-QAIIERAQGKRRVHYD-----FSMSQGLQNPALMAALR-----	293	CC	-----			
Db	273	PADISSITRVPSESEPPALQNLNLSPPLTGTESPPFDLQ-----QWQDLMIMEMOAMEVNT	330	CC	-----			
QY	294	-----PGPPPVFRLTGIGPAPDNDY-LHEV--GCKLAHLAFAIHVEFEYRGFV	340	CC	-----			
Db	331	SASEILYSAAPPGDPPLSTNVSLAPTPINONVSLHQASLGGCSQDFLLPSPEV-----	383	CC	-----			
QY	341	ANTLADASMLASMLERPSEIESVANNSVF-----ELHKLGLR	376	CC	-----			
Db	384	-SLPVASSSTPLPLAPS--NSTSLNSTFGSTNLTGLEFPQOLNLQNTDAGPLPDPGLG	439	CC	-----			
QY	377	PGADKV-----LGVNVNIQIAPEITVQEWSNHNSPPIFLDRFTESLHYKYSTLFDSSL	427	CC	-----			
Db	440	-GLLDEAMLDEISLMLDDEEGFNVPQASOLEEFDSDGLSLD-----SSHSFSSL-SSS	493	CC	-----			
QY	428	EGVPSGQDKVMSEVYLKGQICNVVACDGDRVERHETLSQWRREGSGAAHIGNSNAF	487	CC	-----			
Db	494	EGSSSSSS-----	526	CC	-----			
QY	488	KQASMLL-----FNGGEGYRVEESDGCLM	513	CC	-----			
Db	527	SSDSETLDLEEAEGAVGTOPEYSRCRM	554	CC	-----			
<b>RESULT</b> 2								
ID	CNDL_SCHPO	STANDARD;	PRT;	1158 AA.				
AC	09479;							
DT	20-AUG-2001 (Rel. 40, Created)							
DT	20-AUG-2001 (Rel. 40, Last sequence update)							
DT	20-AUG-2001 (Rel. 40, Last annotation update)							
DE	CONDENSIN COMPLEX SUBUNIT 1 (P128).							
GN	CNDL OR SPBC776.13.							
OS	Schizosaccharomyces pombe (Fission yeast).							
OC	Fungi; Ascomycota; Schizosaccharomyces;							
OC	Schizosaccharomyces; Schizosaccharomyces.							
ON	NCBI_TaxID=48956;							
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 5.8-536; 658-667 AND 1.126-1.138.							
RX	MEDLINE-99415811; Pubmed-104185489;							
RA	Surani T., Yuasa T., Tomonaga T., Dohmae N., Takio K., Yanagida M.;							
RT	"Fission yeast condensin complex: essential roles of non-SMC subunits for condensation and Cdc2 phosphorylation of Cut3/SMC4."							
RL	Genes Dev. 13:2271-2283(1999).							
RN	[2]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=972;							
<b>RESULT</b> 3								
YMBB_YEAST	STANDARD;	PRT;	1420 AA.					
ID	003496; Q04862;							
AC	01-NOV-1997 (Rel. 35, Created)							
DT	01-NOV-1997 (Rel. 35, Last sequence update)							
DT	01-NOV-1997 (Rel. 35, Last annotation update)							
DE	HYPOTHETICAL 163.6 KDA PROTEIN IN PET111-TIF11 INTERGENIC REGION.							

GN	YMR259C OR YMR920_13C OR YMB156_01C.	Db	979 LALQQILVPQYLSGTRDMELQRTLEKKAYKLKLTCCLETCDIPDSI 1038
OS	Saccharomyces cerevisiae (Baker's yeast).	Qy	460 ERHETLSQWRNRFQSGAAGFAAAHIGSNAFKQASMLLALLENGGEGYRVEES ---DGCLM 513
OC	Eukaryota; Fungi; Ascomycota; Saccharomyctina; Saccharomycetes;	Db	1039 LK-DYISSLRNTFIAENNEYVDGSISQLYLAQILDMLL ---KYDTSYIQLDCLL 1089
OC	Saccharomyctinales; Saccharomycetaceae; Saccharomycetes.		
NCBI_TAXID	4932;		
OX			
RN	[1]		
RP	SEQUENCE OF 1-118 FROM N.A.		
RC	STRAIN=S288C / AB972;	RESULT 4	
RA	Lye G., Churcher C.M., Barrell B.G., Rajandream M.A.;	ID POLG_PSBMV	STANDARD; FRT; 3206 AA.
RL	Submitted (MAY-1995) to the EMBL/GenBank/DBJ/GenBank/DBJ/GenBank/DBJ databases.	ID F29152;	
RN	[2]	AC	
RP	SEQUENCE OF 73-1420 FROM N.A.	DT 01-DEC-1992 (Rel. 24. Created)	
RC	STRAIN=S288C / AB972;	DT 01-DEC-1992 (Rel. 24. Last sequence update)	
RA	Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S. V.;	DT 20-AUG-2001 (Rel. 40. Last annotation update)	
RL	Submitted (MAY-1995) to the EMBL/GenBank/DBJ/GenBank/DBJ databases.	DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDa PROTEIN (1.6 kDa); CYTOPLASMIC INCLUSION PROTEIN (C1); 6 KDa PROTEIN (2.6 kDa); GENOME-LINED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA) (EC 3.4.22.44) (4.9 KDa PROTEINASE) (4.9 KDa-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.46); COAT PROTEIN (CP)].	
CC		DE PEAK PROTEIN (CP).	
CC		DE Pea seed-borne mosaic virus (strain DP1).	
CC		OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;	
CC		OC Potyvirus.	
DR	EMBL: Z49260; GAA89242.1; -.	OX NCBI_TaxID:31736;	
DR	SGD: SGD:S0004872; YMR259C.	RN [1]	
KW	Hypothetical protein.	RP SEQUENCE FROM N.A.	
SQ	SEQUENCE 1420 AA; 163576 MW; APBB0CF83CB169D CRC64;	RX MEDLINE=92044431; PubMed=194058;	
CC		RA Johansen E., Rasmussen O.F., Heide M., Borkhardt B.;	
CC		RT "The complete nucleotide sequence of pea seed-borne mosaic virus RNA."	
CC		RT	
CC		RL J. Gen. Virol. 72: 2675-2632 (1991).	
CC		CC -; FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.	
CC		CC -; FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT MAY BE INVOLVED IN REPLICATION.	
CC		CC -; FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.	
CC		CC -; CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HYDROLYSES GLUTAMINYL BONDS, AND ACTIVITY IS FURTHER RESTRICTED BY PREFERENCES FOR THE AMINO ACIDS IN P6 -P1, THAT VARY WITH THE SPECIES OF POTYVIRUS. E.G., GLU-XAA-TVR-XAA-GLN-(SER OR GLY) FOR THE ENZYME FROM TOBACCO ETCH VIRUS. THE NATURAL SUBSTRATE IS THE VIRAL POLYPROTEIN, BUT OTHER PROTEINS AND OLIGOPEPTIDES CONTAINING THE APPROPRIATE CONSENSUS SEQUENCE ARE ALSO CLEAVED.	
CC		CC -; PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.	
CC		CC -; PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOBOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.	
CC		CC -; SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.	
CC		CC -; SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.	
CC		CC -; SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.	
CC		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
CC		CC EMBL: D10130; BAA01726.1; -.	
CC		DR PIR; JQ1331; GNVSPV.	
Qy	14 IMMNEEDDNGMDELLAVIGYKVRSEMPADVAQKLEQLEMMNSVQEDDSLQSLATEV -72	DR MEROPS; C04_001; -.	
Db	533 TSLLSDYERKDAGATVYEF-FTWNGSQRFSIDQTIDILAQMVQNLDNSIG-CAENSIG 590	DR InterPro; IPR001410; DEAD.	
Qy	73 -HYNFAELYTWLDSMUTDNPPSSNAEYDIAKIPDQATIDQFADATSNNOGGGDTY 131	DR InterPro; IPR001650; Helicase_C.	
Db	591 PHEAFLSL-----	DR InterPro; IPR001730; Peptidase_C4.	
Qy	132 TNKRKCSNGNVETTATAESTRHVYLVDSQENGVRVYHALLACAEAQVRENLTVAEALV 191	DR InterPro; IPR001456; Peptidase_C6.	
Db	613 ---SKTISLNLVYVLSWATRNVQHD-----ARGILPEYAA---NCGVPDQYI 657	DR InterPro; IPR002540; Poty_P1.	
Qy	192 KQIGFLAVSOGIGAMRKVATYFAEALARRYKLSPSQSPIDHSLSDTLQMHFYETCPYLF 251	DR InterPro; IPR001592; Poty_coat.	
Db	658 ISHAFRAI-----KEASYLLETILKK-YPLTRIQ--LD-SIGDFTVQ-----STI 700	DR InterPro; IPR001205; RNA_Pol_P3D.	
Qy	252 AHFTANQIALEAFQKKRVEVIDPSMSQGQWPM-----QALALRPGG 296	DR InterPro; IPR001254; Trypsin.	
Db	701 RHSGAQAVIPLGLKA-----FCIRCQLEFPATEELSKVSKLSKTSQHITRRSGG 752		
Qy	297 PPVFRITGIG-----PPAPNFD--YLHVEGC-----SLEG - 429		
Db	753 LPFLVTTVLSAETVKGRPLQKTFENLLVARYLTPHDFDLPQVNA INCNAIYFEP 812		
Qy	322 KL-----AHLAEAATHVEF-----EX 336		
Db	813 KLSVHCTSFVSEALFLALLNFCDIWA1RNCSIMLFTSLQNRIFGKVGRSVSAKLFFTY 872		
Qy	337 RGFVANTLADASMLELRFSEIESVAVNSVFEIHLKLURGPGADKVLGVVNQIKPEI -- 394		
Db	873 SGLROLLNLNSSTAQYSGSERSYQISIF-----LVLNVLLURPTAGY 919		
Qy	395 -----FTVQEESNHNSPFIPLDRFTESHYSTLFD-----SLEG - 429		
Db	920 TGLKRFNVTYECOSNENWKKI-RUMASRVYHMLSENFEETKLLDLASAKQNLHGHJ 978		
Qy	430 -----VP-----SG-----QDK - VMSSEVYLGKQICNWNVACDGPDRV 459		

DR	Pfam; PF00270; DEAD; 1.	Qy	399 EQESNNHNSPIFLDRF---TESLHYYSTLFDSELEGVPSGQDKVMSEVYLGKQICNVVACD 454
DR	Pfam; PF00863; Peptidase_C4; 1.	Db	549 EWESNEESLLEBLARNHNRKPTESI-----ASGGTSFRNKISAKA---QINPALMCD 596
DR	Pfam; PF00851; Peptidase_C6; 1.		
DR	Pfam; PF00767; Ptoty_coat; 1.		
DR	Pfam; PF01577; Ptoty_P1; 1.		
DR	Pfam; PF00680; RNA_dep_pol; 1.		
DR	PRINTS; PRO0966; NIAPOTVPTASE.		
DR	SMART; SM00487; DEADCC; 1.		
DR	SMART; SM00490; HELICC; 1.		
KW	Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;		
KW	Coat protein; Polyprotein; Covalent protein RNA linkage; Helicase;		
KW	ATP-binding.		
FT	CHAIN 1		
FT	CHAIN 2	?	856
FT	CHAIN 3	?	857
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FT	CHAIN 248	?	1102
FT	CHAIN 249	?	1103
FT	CHAIN 250	?	1104
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FT	CHAIN 312	?	1166
FT	CHAIN 313	?	1167
FT	CHAIN 314	?	1168
FT			





DR	Pfam; PF00118; cpn60_TC1; 1.	RA	Highlander S.K., Chidambaram M.J., Engler M.J., Weinstock G.M.; "DNA sequence of the <i>Haemolyticum</i> leukotoxin gene cluster."
DR	PRINTS; PR00298; CHAPERONIN60.	RT	"DNA sequence of the <i>Haemolyticum</i> leukotoxin gene cluster."
DR	PROSITE; PS00304; ICOMPLEXTCPL.	RL	DNA 8-15-28(1989).
DR	PROSITE; PS00296; CHAPERONINS_CPN60; 1.	RN	[3]
Chaperone; ATP-binding; Chloroplast; Chloroplast (POTENTIAL).	Chaperone; ATP-binding; Chloroplast; Chloroplast (POTENTIAL).	RP	SEQUENCE OF 884 953 FROM N.A.
FT TRANSIT	1 ? CHLOROPLAST (POTENTIAL).	RC	STRAIN=SEROTYPE A1 / PHL101;
FT CHAIN	2 ? RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT	RX	MEDLINE=90236888; PubMed=2185213;
FT	580 MW; 16FD34B115E706F7 CRC64;	RA	Highlander S.K., Engler M.J., Weinstock G.M.; Secretion and expression of the <i>Pasteurella haemolytica</i> Leukotoxin.
SEQUENCE	580 AA; 61863 MW; 16FD34B115E706F7 CRC64;	RT	J-Bacteriol. 172:2343-2350(1990).
Query Match	3.7% ; Score 101.5; DB 1; Length 580;	RL	J-Bacteriol. 172:2343-2350(1990).
Best Local Similarity	21.7% ; Pred. No. 7.1; Gaps 24;	CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
Matches 100; Conservative 45; Mismatches 129; Indels 187; Gaps 24;	CC	-1- SUBCELLULAR LOCATION: SECRETED.	
QY	65 SQUATEVHYNPAALEYTILDMSLTDLNPPS-----SNAYE-----DIKATPG-DAIL 110	CC	-1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYCLOYTIC ACTIVITY.
Db	126 SVALEHYH-----LQVTTAGANPQGGDTYTTRKVLCSNSV-----VETTIAA-----178	CC	-1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
QY	111 NQFAIDASSSSNQGGGDTYTTRKVLCSNSV-----VETTIAA-----149	CC	-1- PFM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).
Db	179 N--VASTISAGDNAIGEMIAADALDKVGNSNGVLSIETSTTVEVQSGMEIDRGYISP 235	CC	-1- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
QY	150 ------AESTRHIVLVDQ-----ENGRVHLALLAGAEAVQKENL-----184	CC	-----
Db	236 QFVTNQERLIVYDNCRVLTVDOKIDAIRDIIPLEQVTRNAPNPLITAEDVSSEALATL 295	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch">http://www.isb-sib.ch</a> ).
QY	185 ------TVAEALVQKQIF-----LAVSQTGAMRK 207	CC	-----
Db	296 VVNLKRGVLNVAKIKAPGEGERKSLLQDIAVIVGAEFTAKDLMKVEAVNLGVARK 355	CC	-----
QY	208 V-----ATYFAEALAR-----RIVRLSPSQSPIDHSLSDTLQMHFYETCPYLKFAHFTA 256	CC	-----
Db	356 VTVANNTTLLIADASKDTEIEMIAQQLKELAETD-SYDTEKL-----ERIAKLG 407	CC	-----
QY	257 NQAL-----EARQGKRVHIVDMSMGSQGLWALQMLARLGGPPYFRLLGIGPP 310	CC	-----
Db	408 GVAVIVKVGAAAELEDRKLRIED-----AKNATFAAVEECSIV-----PGG-----448	CC	-----
QY	311 DNFDYLHEVGCKLAHAAIHVPEYRGFVANTLAD-----LDASMLELR-PSEI-----ES 361	CC	-----
Db	449 ------GAALHISSEVPAKE-----LTDAEERKLGADIVMSLRAPCRILADN 492	CC	-----
QY	362 VAVNSVFLHKLGRP-----GAIDKV-----LGVVNQIK 391	CC	-----
Db	493 AGVEGEVIVQRLLGKPFEVGYNAMIDKVENLDAGVIDPAK 533	CC	-----
RESULT	9	CC	-----
ID LKA1_PASHA	STANDARD;	PRT;	953 AA.
AC P1635;			
DT 01-AUG-1990 (Rel. 15, Created)			
DT 01-AUG-1990 (Rel. 15, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE LEUKOTOXIN FROM SEROTYPE A1.			
GN LKTA			
OS <i>Pasteurella haemolytica</i> .			
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC Mannheimia.			
NCBI_TaxID=75985;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=SEROTYPE A1;			
RX MEDLINE=87306837; PubMed=3040588;			
RA Lo, S.Y.C., Strathe, C.A., Shewen, P.E.; "Nucleotide sequence of the leukotoxin genes of <i>Pasteurella haemolytica</i> A1." Int. Immun. 55:1987-1995(1987).			
RT			
RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=SEROTYPE A1; PubMed=2707120;			
RX MEDLINE=89210283; PubMed=2350155;			
RA			
QY	19 EEDDNGNMDDELLAV-----LGKVRSSEMADVAQK-----LEFOLEYMMNSVQYQEDD 63	QY	-----
Db	55 DTEQGNGLQDLVKAABEFLGELEVQERERNNIATAQTSLGTTQIAIGLTERGIVLVSAAQIDK 114	Db	-----
QY	64 LSQL-----ATETVHYNPAELTYWLDMSMUTDNPSSNAEYDIAKPDALINQFAI 115	QY	-----
Db	115 LQKTKAGQALGSAESVQVNANKAKTVLGSQIOLGSVLAGMDL-FALQNNNS-NQHAL 171	Db	-----
QY	116 DSASSNNQGGGGDTYTNNKRIKCSNNEVTT-----	QY	-----

Db	172 AKAG-----LELTNSLIENANSVKTLDDEFGEQTSQFGSSKLQNQKGLGT	215	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
Qy	149 TAESTRHVLVLDQSQENGVRVLYHALLACAEAVQKENLTVAE---ALKVQIGF--LAWSQI	202	CC or send an email to license@isb-sib.ch.
Db	216 LGDKLKNIGGDKAGLGDVSGLSDTQGSGATQA---LVLADKNASTAKVYAGGFLANQVY	271	CC
Qy	203 GAMRK-VATYFAELARRYLTPSPQSPIDHSLSPDTLOMHFYETCPYL----KFAHFT	255	DR EMBL: M84414; AAA35397.1; -
Db	272 GNTIKRASSYT---LAQRVAAGLSSGPVAAILAVSVL--AISPLAPAGIADKFNHAK	325	DR PIR: IP000192; Aminotransf_class_V.
Qy	256 ANQALILEAF-----QGKRVHVIDFSMSQGLQWPAALQALRPGG-----	296	DR Pfam: PF00266; aminotran_5; 1.
Db	326 SLESTAERFKLGVDGNLIAEYQRTGTIDASVY-----AINTALAAATAGGVSAAAG	379	DR PROSITE: PS0395; AA_TRANSFER_CLASS_5; 1.
Qy	297 ----PPVFRITGIGPAPDNFDLYHEVGCKLAIAEAIH---VEFE-----YRGF	339	DR Transferase; Aminotransferase; Pyridoxal phosphate; Peroxisome; Mitochondrion; transit peptide; Alternative initiation.
Db	380 SVIATPIALVSGTITGVISITLQYSKQ---AMEHVNKLNKHIVEWKNNHGNKNYFENCY	437	FT TRANTID 1 23 MITOCHONDRIAL ISOFORM.
Qy	340 VANTLADLDASM-----LELRPSEIATVAVNSVE-----LHKLLGRPAIDKVILGVVNQI	390	FT CHAIN 24 414 SERINE--PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL ISOFORM.
Db	438 DARYLANLQDNMKFLNLN KELQERVIAITQQQWDNNIGDLAGISRLGEKVL-----	490	FT CHAIN 23 414 SERINE--PYRUVATE AMINOTRANSFERASE, PEROXISOMAL ISOFORM.
Qy	391 KPEIPTVVEQESNHNSPIFLDRFTESLHYS---TLEFDLSLEGV---PSQGDQKVMSEYVL	443	FT INIT MET 23 23 FOR PEROXISOMAL ISOFORM.
Db	491 -----SGKAYVDAFEEGKHKIAKDLVQLDSDANGIITDVNSNCKAKTOHILFR	536	FT BINDING 231 231 PYRUVATE PHOSPHATE (BY SIMILARITY).
Qy	444 GKQICNQNVACDGPDRVERHET-----LSQWQRNRFGSA-----GF	477	FT SEQUENCE 414 AA: 45054 MW: 604866DA2EDEDE1 CRC64;
Db	537 -----TPLLTPGEHTERRVYKTYKEYITKUNINRVDWKITDGAASSTEDLTNVQRIGI	591	Query Match 3.7%; Score 101; Pred. No. 4.7;
Qy	478 AAHTGS-NAFKQASMLLA-----FNGGGY-RVEEESDG	510	Best Local Similarity 21.9%; Pred. No. 4.7;
Db	592 ELDNAGNVTKTKEYKIIAKLGEQDDNNFVSGTTEIDGGEGYDRHYSRG	641	Matches 70; Conservative 41; Mismatches 115; Indels 94; Gaps 15;
RESULT 10			
ID	SPY-CALJA	STANDARD	PRT; 414 AA.
AC	P31059;		
DP	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	SERINE--PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.51) (SPT) (ALANINE--GLYOXYLATE AMINOTRANSFERASE)		
DE	(EC 2.6.1.44) (AGT).		
GN	AGXT OR AGT1.		
OS	Callithrix jacchus (Common marmoset).		
CC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Callithrix; Eutheria; Primates; Platyrrhini; Callitrichidae;		
CC	Callithrix.		
CO	NCBI_TaxID:9483;		RESULT 11
RN	[1]	MA2B_FELCA	STANDARD; PRT; 1007 AA.
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92339467; PubMed=11339350;		
RA	Purdue P.E., Lumb M.J., Danpure C.J.;		
RT	"Molecular evolution of alanine/glyoxylate aminotransferase 1 intracellular targeting. Analysis of the marmoset and rabbit genes."		
RL	Eur. J. Biochem. 207:757-766(1992).		
CC	-!- FUNCTION: DUAL METABOLIC ROLES OF GLUCONEOGENESIS (IN THE MITOCHONDRIA) AND GLYOXYLATE DETOXIFICATION (IN THE PROXISOMES).		
CC	-!- CATALYTIC ACTIVITY: L-SERINE + PYRUVATE = 3-HYDROXYPYRUVATE +		
CC	-!- CATALYTIC ACTIVITY: L-ALANINE + GLYOXYLATE = PYRUVATE + GLYCINE.		
CC	-!- COFACTOR: PYRIDOXAL PHOSPHATE AND PEROXISOMAL.		
CC	-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX AND PEROXISOMAL-PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.		
CC	-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.		
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CC	CC RELEASED DURING GLYCOPROTEIN TURNOVER (BY SIMILARITY).		

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING  
 CC ALPHA-D-MANNOSE RESIDUES IN ALPHA-D-MANNOSIDES.  
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL.  
 CC -!- PTM: PROCESSED INTO 3 PEPTIDES OF 72 KDA, 41 KDA AND 12 KDA.  
 CC -!- DISEASE: 35. MANB ARE THE CAUSE OF LYSOSMAL ALPHA-  
 CC MANNOSIDOSIS, A LYSOSOMAL SPORADIC DISEASE CHARACTERIZED BY  
 ACCUMULATION OF UNBRANCHED OLIGOSACCHARIDES CHAINS.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF010191; AAB97672.1; -.  
 DR AF010192; AAB97733.1; -.  
 DR InterPro; IPD000502; Glyco\_hydro\_38.  
 DR Pfam; PF01074; Glyco\_hydro\_38; 1.  
 DR SIGNAL; SIGNAL1; 50.  
 FT KW BY SIMILARITY.  
 FT CHAIN 51 1007 LYSOSOMAL ALPHA-MANNOSIDASE.  
 SEQUENCE 1007 AA; 113230 MW; C064A8168F5DC20A CRC64; 32;

Query Match 3.6%; Score: 100; DB: 1; Length: 1007;  
 Best Local Similarity 19.0%; Pred. No: 20;  
 Matches 104; Conservative 80; Mismatches 185; Indels 178; Gaps 32;

Qy 74 YNPAAELYTWLDSM-----LTDLNPPSSNAEYDLKAIKGDAILNQFAIDSASSNNQGGGG 127  
 Db 262 YNPEPKLW-DTICADPFPVDRSPYNAE-----ELVNYF-LOLATAQ-----G 305  
 Qy 128 DTYTTNKRKLCNSGNGVETTAT--AESTRHVVLVDSQE--NG-VRLVHALLAC-AEAV 179  
 Db 306 QHFRNTNTIMTGSDFQYENANMWMERLQLQVNAQOQNSRNRVLYSTPACYLWEI 365  
 Qy 180 QKRNNTVAEALYRQIQFIAVSQGAMKRVTAFAEALRQYRRLSPSQSPIDHSLSLSDTO 239  
 Db 366 NKRNLWTS--VKQDDDFPYAD-GPHOFWSGYFSSRPALKRY-----ERLS 407  
 Qy 240 MHYETC-----PYLKFAHTANQALI-----EAFOGKKRVHYI-DFSMSQ 279  
 Db 408 YNFLQVNQLEALAGPAAVNPQGSGSAPLNQAMAVLQHIDAVSCTSKHQVADDYARQL 467  
 Qy 280 GLQWP-----ALNOALALRPQGPVFRLTGIGPPAPDNFDYLHEVG---CKLAHLAE--- 328  
 Db 468 AAGWDPCPEVLSNALA-----RLSG-----SKEDTYCRLNLYNSVCPQLSQTAKNEQV 514  
 Qy 329 -----AIVHDFEYRQFV-----NFIADLDSLME-----LRISEIESYAVN 365  
 Db 515 TIYNPLGRKIDMVRPLPVSKHGFVVRDPNPTVPSDVVILPSDQGELFLFASVPLGF- 573  
 Qy 366 SVPFLHKLG-RPG-----IDKVLGVVNO-----IRPEIITVVEOBNSHNSPIF 409  
 Db 574 SIVYSVQSPQGPDRPHAKHPQPRSPQRSPRLAQNEHTRARPDPTGLLVENIDONLL 633  
 Qy 410 LDRFTESLHY-----STLFDSEGV-----PSGQDKYMSSEYVLGKQICCNVYACDGPDRVE 460  
 Db 634 PVR--QAFWYVNASVGNLNLSTOVSGAYIFRPQEKPLMVSIAQTLVKT----PLVQE 686  
 Qy 461 RHETLSQWRNPGSAGTAAGHGSNAFKQASMLAIFNGGQYRVRQESDGLMLGHTRP 520  
 Db 687 VHQNEFSAW-----CSQVRLYRGQRHLELE-----WTVGP 716  
 Qy 521 LIATSAW 527  
 Db 717 IPVGDGW 723

YY02\_METJA STANDARD PRT: 1181 AA.  
 YY02\_METJA ID YY02\_METJA  
 YY02\_METJA AC 060301;  
 YY02\_METJA DR 01-NOV-1997 (Rel. 35 Created)  
 YY02\_METJA DT 01-NOV-1997 (Rel. 35 Last sequence update)  
 YY02\_METJA DT 20-AUG-2001 (Rel. 40 Last annotation update)  
 YY02\_METJA DE HYPOTHETICAL PROTEIN MJEC502.  
 YY02\_METJA OS Methanococcus lannaschii.  
 YY02\_METJA OC Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;  
 YY02\_METJA OC Methanococcus;  
 YY02\_METJA OX NCBI\_TAXID=2190;  
 YY02\_METJA RN [1]  
 YY02\_METJA RP SEQUENCE FROM N.A.  
 YY02\_METJA RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 YY02\_METJA RX MEDLINE=96137999; PubMed=1688087;  
 YY02\_METJA RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 YY02\_METJA RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 YY02\_METJA RA Overholtka R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 YY02\_METJA RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen A.,  
 YY02\_METJA RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 YY02\_METJA RA Cotton M.D., Roberts K.M., Hurst J.M., Kaine B.P., Borodovsky M.,  
 YY02\_METJA RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 YY02\_METJA RT Complete genome sequence of the methanogenic archaeon, Methanococcus  
 YY02\_METJA RT lannaschii";  
 YY02\_METJA RL Science 273:1058-1073(1996).  
 YY02\_METJA CC -!- SIMILARITY: WEAK IN THE C-TERMINUS, TO ADENINE-SPECIFIC  
 YY02\_METJA CC METHYLTRANSFERASES.  
 YY02\_METJA -----  
 YY02\_METJA This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 YY02\_METJA CC -----  
 YY02\_METJA DR EMBL; L77119; AAC37000.1; -.  
 YY02\_METJA DR HSSP; P14385; IAJQV.  
 YY02\_METJA DR TIGR; MJEC502; -.  
 YY02\_METJA DR InterPro; IPR02296; N12N6\_mtfrase.  
 YY02\_METJA DR PRINTS; PRO0507; N12N6MTTFASE.  
 YY02\_METJA DR PROSITE; PS0092; N6\_MTASE; 1.  
 YY02\_METJA DR TRANSMEM 837 857 PCTENTAL.  
 YY02\_METJA SQ SEQUENCE 1181 AA; 138438 MW; 9F961D8F8C6A4BDD CRC64;  
 YY02\_METJA DR -----  
 YY02\_METJA DR Query Match 3.6%; Score: 99.5; DB: 1; Length: 1181;  
 YY02\_METJA DR Best Local Similarity 20.3%; Pred. No: 28;  
 YY02\_METJA DR Matches 112; Conservative 85; Mismatches 199; Indels 157; Gaps 29;  
 YY02\_METJA DR -----  
 YY02\_METJA Qy 24 NGMDELLAV--LGKVRSSEMADVQKLEOLEVMVSNVQEDDLSQLQATEVHYNPAELY 80  
 YY02\_METJA Db 524 SALKELQIKKRIVYLRL-EEMDIYK--EKLGIILNLYGVDDIDIAVEI----AKLR 574  
 YY02\_METJA Qy 81 TWLSDMSLTDLNPSSNAEYDLKAIP-GDAILNQFALDSASSSNQGGDITYTTNKRKCS 139  
 YY02\_METJA Db 575 LWL-ALIENL-----DVEALKRGEVLPNIEW-----VRCG 605  
 YY02\_METJA Qy 140 NGVVEETATAESTRHVLYDQSQENGVRLYHALLACAEAVOKENLUTVA-FALVKOIGFLA 198  
 YY02\_METJA Db 606 NSLVGWTDENIKLQLS-SYLCDNVRIMCVLRLQVLYHALLACAEAVOKENLUTVA-FALVKOIGFLA 198  
 YY02\_METJA Qy 199 VSQIGAMRKVATYFAAFLARRIYRULSPS-OSPIDHSLSDFLQMHFYYTCPYKFAH----254  
 YY02\_METJA Db 666 DNYVEYAH-----LLVEVYPRSHGLKANLKLKELDEIRDSEYESPAYAEIYQN 716  
 YY02\_METJA Qy 255 -----TANOQIALEAFQGKKRVRH-YIDFMSMSQGLQWPAIMQALALRPGGPPVFRL 302  
 YY02\_METJA Db 717 GNNKKNGKSKRNKRVRVEEFEKLKEFWKIDFG----WIKBEGFDVIGNPPYGNL 770

DR	SMART;	SM00479: EXOIII; 1.
DR	SMART;	SM00481; POLIAC; 1.
KW	Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;	
KW	Nuclease; Exonuclease;	
FT	DOMAIN	4.20
FT	CONFILCT	584
FT	CONFILCT	207
FT	CONFILCT	952
FT	CONFILCT	1049
FT	CONFILCT	1035
FT	CONFILCT	1147
FT	CONFILCT	1260
FT	CONFILCT	1409
FT	CONFILCT	1436
SQ	SEQUENCE	AA;
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RC	TISSUE-Liver;	PHBC_RHET	
RX	MEDLINS=94/22101; PubMed=8168541;	ID PHBC_RHET	STANDARD;
RA	Purdue P.E., Dangpure C.J.;	AC 052728;	PRT; 636 AA.
RT	"Molecular evolution of alanine/glyoxylate aminotransferase 1 intracellular targeting. Analysis of the feline gene."	DT 30-MAY-2000 (Rel. 39, Created)	
RT		DT 30-MAY-2000 (Rel. 39, Last sequence update)	
RL	RJ. J. Blochem. 221:53-62 (1994).	DT 20-AUG-2001 (Rel. 40, Last annotation update)	
CC	-1- FUNCTION: DUAL METABOLIC ROLES OF GLUCONEOGENESIS (IN THE MITOCHONDRIA) AND GLYOXYLATE DEOXIDIFICATION (IN THE PEROXISOMES).	DE POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.1.) (POLY (3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY (3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHB SYNTHASE) (PHA SYNTHASE).	
CC	-1- CATALYTIC ACTIVITY: L-SERINE + PYRUVATE = 3-HYDROXYPYRUVATE + L-ALANINE.	DE POLYHYDROXYALKANOIC ACID SYNTHASE).	
CC	-1- CATALYTIC ACTIVITY: L-ALANINE + GLYOXYLATE = PYRUVATE + GLYCINE.	DE PHB OR PHAC.	
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.	OS Rhizobium etli.	
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (>90%) AND PEROXISOMAL.	OC Rhizobiaceae; Proteobacteria; alpha subdivision; Rhizobiaceae group;	
CC	-1- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.	OC Rhizobium.	
CC		OX NCBI_TaxID=29449; [1]	
CC		RN	
CC		RP	SEQUENCE FROM N.A.
CC		RC	STRAIN=CE 3;
CC		RC	MEDLINE=6198168; PubMed=8626293;
CC		RA	Cevallos M.A., Encarnacion S., Leija A., Mora Y., Mora J.;
CC		RA	"Genetic and physiologic characterization of a Rhizobium etli mutant strain unable to synthesize poly-beta-hydroxybutyrate."
CC		RT	J. Bacteriol. 178:1646-1654 (1996).
CC		RL	
CC		CC	-- FUNCTION: POLYMERIZES D(-)-3-HYDROXYBUTYRYL-COA TO CREATE PHB WHICH CONSISTS OF THOUSANDS OF HYDROXYBUTYRATE MOLECULES LINKED END TO END. PHB SERVES AS AN INTRACELLULAR ENERGY RESERVE MATERIAL.
CC		CC	WHEN CELLS GROW UNDER CONDITIONS OF NUTRIENT LIMITATION.
CC		CC	-- PATHWAY: THIRD STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
CC		CC	-- SUBCELLULAR LOCATION: CYTOSOLIC (BY SIMILARITY).
CC		CC	-- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC		CC	--
DR	EMBL: X75923; CAA53527 1; [1]	CC	--
DR	InterPro: IPR00192; Aminotransf_class_V.	CC	--
DR	PFAM: PF00266; aminotran5; 1.	CC	--
DR	PROSITE: PS00342; MICROBODIES_CTER; 1.	CC	--
DR	PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.	CC	--
KW	Transf erase; Aminotransferase; Pyridoxal phosphate; Peroxisome;	CC	--
KW	Mitochondrion; Transit peptide; Alternative initiation	CC	--
FT	TRANSIT 1 23 MITOCHONDRION (BY SIMILARITY).	CC	--
FT	CHAIN 24 414 SERINE-PYRUVATE AMINOTRANSFERASE,	CC	--
FT	CHAIN 23 414 MITOCHONDRIAL ISOFORM.	CC	--
FT	INIT_MET 23 23 SERINE-PYRUVATE AMINOTRANSFERASE,	CC	--
FT	BINDING 231 231 PEROXISOMAL ISOFORM.	CC	--
FT	SITE 412 414 PYRIDOXAL PHOSPHATE (BY SIMILARITY).	CC	--
FT	SITE 414 414 MICROBODY TARGETING SIGNAL (BY SIMILARITY).	CC	--
SQ	SEQUENCE 414 AA; 45507 MW; 0D1B01E09A198B3 CRC64;	DR	U30612; AAB05020; 1;
		DR	InterPro; IPR000073; Abhydrolase.
		DR	Pfam; PF00561; abhydrolase_1.
		KW	PHB biosynthesis; transferase; Acyltransferase.
		FT	ACT_SITE 373 373 POTENTIAL.
		SQ	SEQUENCE 636 AA; 71935 MW; DD370C10EC89D12 CRC64;
Qy	292 LRPGGPVFRATGIGP--AP-----DNFDYHEVGCKLAHIAEAATHEFEYERGFYA 341	Query Match	3.6%; Score 99; DB 1; Length 636;
Best Local Similarity	21.9%	Best Local Similarity	21.6%; Pred. No. 12;
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Qy	342 NTL-----ADLDASMLE-LRPSSETESAVAVNSVF-----ELHKLGLRPG 378	Qy	15 MMMNEEDDNGMDDELLAVLGKVKRSSEMAADVAQKLEQLEMMNSNVOEDDSLQ-----AT 69
Db	94 NPLTAISGGSGHCALEAALNILEGDPFVVGNCIWIQGKQADIGERICARVHMIKDG 153	Db	287 ETVLKRPLLJCPPRINKFVTLDNPKSFVIKWCVDQGQTVFVSWNPDGRHAEKDWAAY 346
Qy	379 ---ALDKVLGVNVQNIKPEITVVEQESNNNSPIFLDRFTESLHYSTLF---DSLEGV 430	Qy	105 PGDAILNQPAIDSSASSNSOGGGDTYTPNKRKCSNGVETTAETRHYLVLVDSEN 164
Db	154 NYHTQLEELDAAQKPVLFQFLTQEGSSSVQLPDGYGELCHRYNCULLVDSVASYLCT 213	Db	347 AREGI-DPALETEKA-----TGEKEVNAVGVYCVGFTLAAATLH--AKEK 390
Qy	431 P-----SCQDKVNS-----EVYLG-KQICANV 451	Qy	165 GVRVHALLACAEA-----VOKENLTVAEAALYKQIGFL-----AVSQIGAMR 206
Db	214 PIYMDQGIVDLYSGSQKVNLSSQGPTSLISFSKAKNKKYTRKTPKVPSYFLDMKWLANIW 273	Db	391 NKRTKATLEFTQDFTHGDLKVFVDEQLAALIEEHNMQAAGYLGDGSKMSMAFNMLRASE 450
Qy	452 ACDGPDRVERHET--LSQWNRNREGSAGFAAHIGSNFAKASMILLALFNG---GEGRYRE 506	Qy	207 KVATVFAEALARRYRLSPSQSPIDHSL---SDTLMQ-----HFYETCPYLKFAHFTAN 257
Db	274 GCDGPRIYHTTPVSLYISRESLALIAEQGL--ENSWR9HRETRYAYLHGRQLQGLQI 332		
Qy	507 ESDGCLMLGHTRPLIATSA 526		

Db	451	LIWPYFVNSYLK-----GQEPLPFDLLFWNADSTRMAAAANHAFYLRNCYLRNA-LTQN	502
Qy	258	QALEAFQGK-----RVHYIDFSMSQGLQWPAALALR-PGGPPYFRLTGIGPPA-	309
Db	503	EMILD---GKRISLKDVKIPYLNLATREDHTAPAKSVFLGSRFGGKVEFVVTGSHIAG	559
Qy	310	----PDNFYD 315	
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Search completed: May 8, 2002, 11:11:55  
Job time: 215 sec